

**WEST**

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L2: Entry 3 of 3

File: USPT

Oct 19, 1999

DOCUMENT-IDENTIFIER: US 5968744 A  
TITLE: Human cornichon molecule

US Patent No. (1):  
5968744

Detailed Description Text (59):

In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences encoding CORN may be ligated to a heterologous sequence to encode a fusion protein. For example, to screen peptide libraries for inhibitors of CORN activity, it may be useful to encode a chimeric CORN protein that can be recognized by a commercially available antibody. A fusion protein may also be engineered to contain a cleavage site located between the CORN encoding sequence and the heterologous protein sequence, so that CORN may be cleaved and purified away from the heterologous moiety.

Detailed Description Text (66):

In bacterial systems, a number of expression vectors may be selected depending upon the use intended for CORN. For example, when large quantities of CORN are needed for the induction of antibodies, vectors which direct high level expression of fusion proteins that are readily purified may be used. Such vectors include, but are not limited to, the multifunctional E. coli cloning and expression vectors such as Bluescript.RTM. (Stratagene), in which the sequence encoding CORN may be ligated into the vector in frame with sequences for the amino-terminal Met and the subsequent 7 residues of .beta.-galactosidase so that a hybrid protein is produced; pIN vectors (Van Heeke, G. and S. M. Schuster (1989) J. Biol. Chem. 264:5503-5509); and the like. pGEX vectors (Promega, Madison, Wis.) may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. Proteins made in such systems may be designed to include heparin, thrombin, or factor XA protease cleavage sites so that the cloned polypeptide of interest can be released from the GST moiety at will.

Detailed Description Text (81):

Host cells transformed with nucleotide sequences encoding CORN may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a transformed cell may be secreted or contained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides which encode CORN may be designed to contain signal sequences which direct secretion of CORN through a prokaryotic or eukaryotic cell membrane. Other constructions may be used to join sequences encoding CORN to nucleotide sequence encoding a polypeptide domain which will facilitate purification of soluble proteins. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp., Seattle, Wash.). The inclusion of cleavable linker sequences such as those specific for Factor XA or enterokinase (Invitrogen, San Diego, Calif.) between the purification domain and CORN may be used to facilitate purification. One such expression vector provides for expression of a fusion protein containing CORN and a nucleic acid encoding 6 histidine residues preceding a thioredoxin or an enterokinase cleavage site. The histidine residues facilitate purification on IMAC (immobilized metal ion affinity chromatography as described in Porath, J. et al. (1992, Prot. Exp. Purif. 3: 263-281) while the enterokinase cleavage site provides a means for purifying CORN from the fusion protein. A discussion of

vectors which contain fusion proteins is provided in Kroll, D. J. et al. (1993; DNA Cell Biol. 12:441-453).

Detailed Description Text (194):

Induction of an isolated, transformed bacterial strain with IPTG using standard methods produces a fusion protein which consists of the first eight residues of .beta.-galactosidase, about 5 to 15 residues of linker, and the full length protein. The signal residues direct the secretion of CORN into the bacterial growth media which can be used directly in the following assay for activity.

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DOCUMENT-IDENTIFIER: US 5968744 A  
TITLE: Human cornichon molecule

US Patent No. (1):  
5968744

Brief Summary Text (4):

Differentiation of tissues and determination of body plan in metazoans appears to be rooted in the synthesis of critical extracellular and intracellular proteins during oogenesis and embryogenesis. Determination of body plan is encrypted within embryonic cell lineages, and the fate of specific embryonic cell lineages is determined before fertilization, during oogenesis.

Brief Summary Text (5):

Oogenesis and embryogenesis are regulated by interactions between environmental, extracellular, and intracellular signals. Changes in signaling pathways caused by genetic mutation or biochemical modification can affect oogenesis and embryogenesis in a number of ways. Specifically, these changes may result in the failure of spermatozoa to fertilize the egg, in the premature death of the embryo, and in morphological changes during embryogenesis and during ontogeny.

Brief Summary Text (6):

Signaling pathways have been extensively studied during oogenesis and embryogenesis of the fruit fly, *Drosophila melanogaster*. Soon after fertilization, the *Drosophila* embryo has two axes of polarity, the anterior-posterior axis and the dorsal-ventral axis. These axes of polarity have been observed in all other metazoan embryos thus far studied. The shape of the *Drosophila* egg shows dorsal-ventral polarity at the time it is laid. Genetic studies have shown that three sequential signaling pathways establish the dorsal-ventral axis in the *Drosophila* embryo. The first of these signaling pathways takes place during oogenesis, when the germline-derived oocyte is surrounded by an epithelium of somatically-derived follicle cells. The follicle cells later secrete components of the eggshell. The oocyte produces a dorsalizing signaling ligand that is received by receptors on neighboring follicle cells and defines the polarity of both the embryo and the eggshell. The proposed ligand and receptor in this pathway are encoded by the genes *gurken* and *torpedo*, which are members of the transforming growth factor- $\alpha$  and the epidermal growth factor-receptor families, respectively. Spatial localization of the signal is achieved by localizing *gurken* mRNA to the dorsal anterior side of the oocyte. This is proximal to the asymmetrically positioned dorsal-anterior-localized oocyte nucleus (Morisato, D. and Anderson, K. V. (1995) *Annu. Rev. Genet.* 29:371-399).

Brief Summary Text (7):

A number of other genes are also required to ensure correct dorsalization of the oocyte. One of the eight which has been identified is *cornichon* (Morisato and Anderson (supra)). The predicted *cornichon* translation product is a 144 amino acid residue hydrophobic protein. Hydrophobic residues are clustered at three distinct regions: the N-terminus, the central region, and the C-terminus of the molecule. There are no putative transmembrane or signal sequences (Roth, S. et al. (1995) *Cell* 81:967-978). *cornichon* is thought to be involved in the membrane localization or proper activation of the *gurken* protein (Morisato and Anderson, supra).

Detailed Description Text (55):

Capillary electrophoresis systems which are commercially available may be used to analyze the size or confirm the nucleotide sequence of sequencing or PCR products. In particular, capillary sequencing may employ flowable polymers for electrophoretic

separation, four different fluorescent dyes (one for each nucleotide) which are laser activated, and detection of the emitted wavelengths by a charge coupled device camera. Output/light intensity may be converted to electrical signal using appropriate software (e.g. Genotype.TM. and Sequence Navigator.TM., Perkin Elmer) and the entire process from loading of samples to computer analysis and electronic data display may be computer controlled. Capillary electrophoresis is especially preferable for the sequencing of small pieces of DNA which might be present in limited amounts in a particular sample.

Detailed Description Text (72):

Specific initiation signals may also be used to achieve more efficient translation of sequences encoding CORN. Such signals include the ATG initiation codon and adjacent sequences. In cases where sequences encoding CORN, its initiation codon, and upstream sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a fragment thereof, is inserted, exogenous translational control signals including the ATG initiation codon should be provided. Furthermore, the initiation codon should be in the correct reading frame to ensure translation of the entire insert. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers which are appropriate for the particular cell system which is used, such as those described in the literature (Scharf, D. et al. (1994) Results Probi. Cell Differ. 20:125-162).

Detailed Description Text (81):

Host cells transformed with nucleotide sequences encoding CORN may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a transformed cell may be secreted or contained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides which encode CORN may be designed to contain signal sequences which direct secretion of CORN through a prokaryotic or eukaryotic cell membrane. Other constructions may be used to join sequences encoding CORN to nucleotide sequence encoding a polypeptide domain which will facilitate purification of soluble proteins. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp., Seattle, Wash.). The inclusion of cleavable linker sequences such as those specific for Factor XA or enterokinase (Invitrogen, San Diego, Calif.) between the purification domain and CORN may be used to facilitate purification. One such expression vector provides for expression of a fusion protein containing CORN and a nucleic acid encoding 6 histidine residues preceding a thioredoxin or an enterokinase cleavage site. The histidine residues facilitate purification on IMAC (immobilized metal ion affinity chromatography as described in Porath, J. et al. (1992, Prot. Exp. Purif. 3: 263-281) while the enterokinase cleavage site provides a means for purifying CORN from the fusion protein. A discussion of vectors which contain fusion proteins is provided in Kroll, D. J. et al. (1993; DNA Cell Biol. 12:441-453).

Detailed Description Text (108):

As mentioned above, modifications of gene expression can be obtained by designing complementary sequences or antisense molecules (DNA, RNA, or PNA) to the control, 5' or regulatory regions of the gene encoding CORN (signal sequence, promoters, enhancers, and introns). Oligonucleotides derived from the transcription initiation site, e.g., between positions -10 and +10 from the start site, are preferred. Similarly, inhibition can be achieved using "triple helix" base-pairing methodology. Triple helix pairing is useful because it causes inhibition of the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors, or regulatory molecules. Recent therapeutic advances using triplex DNA have been described in the literature (Gee, J. E. et al. (1994) In: Huber, B. E. and B. I. Carr, Molecular and Immunologic Approaches, Futura Publishing Co., Mt. Kisco, N.Y.). The complementary sequence or antisense molecule may also be designed to block translation of mRNA by preventing the transcript from binding to ribosomes.

Detailed Description Text (140):

In a particular aspect, the nucleotide sequences encoding CORN may be useful in assays that detect activation or induction of various cancers, particularly those mentioned above. The nucleotide sequences encoding CORN may be labeled by standard methods, and added to a fluid or tissue sample from a patient under conditions suitable for the

formation of hybridization complexes. After a suitable incubation period, the sample is washed and the signal is quantitated and compared with a standard value. If the amount of signal in the biopsied or extracted sample is significantly altered from that of a comparable control sample, the nucleotide sequences have hybridized with nucleotide sequences in the sample, and the presence of altered levels of nucleotide sequences encoding CORN in the sample indicates the presence of the associated disease. Such assays may also be used to evaluate the efficacy of a particular therapeutic treatment regimen in animal studies, in clinical trials, or in monitoring the treatment of an individual patient.

Detailed Description Text (186):

The DNA from each digest is fractionated on a 0.7 percent agarose gel and transferred to nylon membranes (Nytran Plus, Schleicher & Schuell, Durham, N.H.). Hybridization is carried out for 16 hours at 40.degree. C. To remove nonspecific signals, blots are sequentially washed at room temperature under increasingly stringent conditions up to 0.1.times.saline sodium citrate and 0.5% sodium dodecyl sulfate. After XOMAT AR.TM. film (Kodak, Rochester, N.Y.) is exposed to the blots in a Phosphoimager cassette (Molecular Dynamics, Sunnyvale, Calif.) for several hours, hybridization patterns are compared visually.

Detailed Description Text (194):

Induction of an isolated, transformed bacterial strain with IPTG using standard methods produces a fusion protein which consists of the first eight residues of .beta.-galactosidase, about 5 to 15 residues of linker, and the full length protein. The signal residues direct the secretion of CORN into the bacterial growth media which can be used directly in the following assay for activity.

<first sequence: ss.P\_AAZ11186 (length = 1033)  
<second sequence: ss.DNA23330 (length = 1333)  
  
<991 matches in an overlap of 999: 99.20 percent similarity  
<gaps in first sequence: 0, gaps in second sequence: 0  
<score: 2973 (match = 3, mismatch = 0, gap penalty = 8 + 1 per base)  
<endgaps not penalized

GenBank (Release 135, apr 2003)[May 6 11:28:38 2003]: 1 sequence found

P\_AAZ11186 Gene encoding transmembrane domain containing protein clone HP02239.  
033 bp, DNA, PAT 04-NOV-1999  
ACCESSION P\_AAZ11186  
KEYWORDS Transmembrane domain containing protein; human; antibody production;  
interaction assay; diagnosis; nutritional activity; cytokine; cell  
proliferation; cell differentiation activity; immune stimulant;  
immune suppressant; haematopoiesis regulator; tissue growth  
activity; activin; inhibin activity; chemotaxis; chemokinesis;  
haemostasis; thrombolysis; anti-inflammatory; cadherin; tumour  
invasion suppressor; tumour inhibitor; patent; GENESEQ patentdb.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens.  
REFERENCE 1 (bases 1 to 1033)  
AUTHORS Kato,S., Kimura,T., Nakamura,N., Sekine,S.  
TITLE New proteins and DNA useful for preventing tumours  
JOURNAL Patent: WO9943802-A2; Filing Date: 25-FEB-1999; 99WO-JP00875;  
Publication Date: 02-SEP-1999; Priority: 27-FEB-1998;  
98JP-0046607; Assignee: (PROT-) PROTEGENE INC. (SAGA ) SAGAMI CHEM  
RES CENT; Cross Reference: WPI; 1999-527617/44. P-PSDB; AAY32925;  
Patent Format: Claim 4; Page 85-86; 96pp; English.  
COMMENT This sequence encodes a human transmembrane protein of the  
invention. The DNAs are useful for expressing recombinant protein  
for analysis, characterisation or therapeutic use, and are useful as  
markers for tissues in which the corresponding protein is  
preferentially expressed. They are also useful as molecular weight  
markers on Southern gels, as chromosome markers or tags (when  
labelled) to identify potential genetic disorders, as probes to  
hybridise and thus discover novel, related DNA sequences, as a  
source of PCR primers for genetic fingerprinting, as probes to  
subtract-out known sequences in the process of discovering other  
novel DNAs, for selecting and making oligomers for attachment to a  
gene chip or other support, including for examination of expression  
patterns, to raise anti-protein antibodies using DNA immunisation  
techniques, and as an antigen to raise anti-DNA antibodies or elicit  
another immune response. Where the DNA encodes a protein which binds  
to another protein (e.g. in a receptor-ligand interaction), the DNA  
can also be used in interaction trap assays to identify DNAs  
encoding the other protein with which binding occurs or to identify  
inhibitors of the binding interaction. The DNAs and proteins can  
have e.g. nutritional activity, cytokine and cell  
proliferation/differentiation activity, immune stimulating (e.g. as  
vaccines) or suppressing activity, haematopoiesis regulating  
activity, tissue growth activity, activin/inhibin activity,  
chemotactic/chemokinetic activity, haemostatic and thrombolytic  
activity, receptor/ligand activity, anti-inflammatory activity,  
cadherin/tumour invasion suppressor activity, and tumour inhibition  
activity.  
FEATURES Location/Qualifiers

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                  /product= HP02239 protein
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ORIGIN

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                  ** * * * *****
ss.DNA23330          GCCCACGCGTCCGATGGCGTTCACGT
                      10      20

          70      80      90     100     110     120
ss.P_AAZ11186 TCGCGGCCTTCTGCTACATGCTGGCGCTGCTGCTCACTGCCGCGCTCATCTTCTTCGCCA
                  *****
ss.DNA23330      TCGCGGCCTTCTGCTACATGCTGGCGCTGCTGCTCACTGCCGCGCTCATCTTCTTCGCCA
                  30      40      50      60      70      80

          130     140     150     160     170     180
ss.P_AAZ11186 TTTGGCACATTATAGCATTGTGATGAGCTGAAGACTGATTACAAGAATCCTATAGACCAGT
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ss.DNA23330      TTTGGCACATTATAGCATTGTGATGAGCTGAAGACTGATTACAAGAATCCTATAGACCAGT
                  90      100     110     120     130     140

          190     200     210     220     230     240
ss.P_AAZ11186 GTAATACCCTGAATCCCCTTGTACTCCCAGAGTACCTCATCCACGCTTTCTTCTGTGTCA
                  *****
ss.DNA23330      GTAATACCCTGAATCCCCTTGTACTCCCAGAGTACCTCATCCACGCTTTCTTCTGTGTCA
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          250     260     270     280     290     300
ss.P_AAZ11186 TGTTTCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATATGCCCCTCTTGGCATATC
                  *****
ss.DNA23330      TGTTTCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATATGCCCCTCTTGGCATATC
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          310     320     330     340     350     360
ss.P_AAZ11186 ATATTTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCCAGGACTCTATGACCCTACAA
                  *****
ss.DNA23330      ATATTTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCCAGGACTCTATGACCCTACAA
                  270     280     290     300     310     320

          370     380     390     400     410     420
ss.P_AAZ11186 CCATCATGAATGCAGATATTCTAGCATATTGTCAGAAGGAAGGATGGTGCAAATTAGCTT
                  *****
ss.DNA23330      CCATCATGAATGCAGATATTCTAGCATATTGTCAGAAGGAAGGATGGTGCAAATTAGCTT
                  330     340     350     360     370     380

          430     440     450     460     470     480
ss.P_AAZ11186 TTTATCTTCTAGCATTTTTTTTACTACCTATATGGCATGATCTATGTTTGGTGAGCTCTT
                  *****
ss.DNA23330      TTTATCTTCTAGCATTTTTTTTACTACCTATATGGCATGATCTATGTTTGGTGAGCTCTT
                  390     400     410     420     430     440

          490     500     510     520     530     540
ss.P_AAZ11186 AGAACAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAAGCCACCAAATGAAGG
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ss.DNA23330      AGAACAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAAGCCACCAAATGAAGG

```

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	550	560	570	580	590	600
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	*****					
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	610	620	630	640	650	660
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	*****					
ss.DNA23330	AAAATGACTCCTTATTTTTTAAATGTTTCCACATTTTTGCTTGTGGAAAGACTGTTTCA					
	570	580	590	600	610	620
	670	680	690	700	710	720
ss.P_AAZ11186	TATGTTATACTCAGATAAAGATTTTTAAATGGTATTACGTATAAATTAATAAAATGATT					
	*****					
ss.DNA23330	TATGTTATACTCAGATAAAGATTTTTAAATGGTATTACGTATAAATTAATAAAATGATT					
	630	640	650	660	670	680
	730	740	750	760	770	780
ss.P_AAZ11186	ACCTCTGGTGTGACAGGTTTGAACCTGCACTTCTTAAGGAACAGCCATAATCCTCTGAA					
	*****					
ss.DNA23330	ACCTCTGGTGTGACAGGTTTGAACCTGCACTTCTTAAGGAACAGCCATAATCCTCTGAA					
	690	700	710	720	730	740
	790	800	810	820	830	840
ss.P_AAZ11186	TGATGCATTAATTACTGACTGTCCTAGTACATTGGAAGCTTTTGTATTAGGAACCTTGTA					
	*****					
ss.DNA23330	TGATGCATTAATTACTGACTGTCCTAGTACATTGGAAGCTTTTGTATTAGGAACCTTGTA					
	750	760	770	780	790	800
	850	860	870	880	890	900
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	*****					
ss.DNA23330	GGGCTCATTTTGGTTTCATTGAAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGT					
	810	820	830	840	850	860
	910	920	930	940	950	960
ss.P_AAZ11186	GCTTCTGATGAAGTGAAATGTATATCTGACTAGTGGGAACTTCATGGGTTTCCTCATC					
	*****					
ss.DNA23330	GCTTCTGATGAAGTGAAATGTATATCTGACTAGTGGGAACTTCATGGGTTTCCTCATC					
	870	880	890	900	910	920
	970	980	990	1000	1010	1020
ss.P_AAZ11186	TGTCATGTCGATGATTATATATGGATACATTTACAAAAATAAAAAGCGGGAATTTCCCT					
	*****					
ss.DNA23330	TGTCATGTCGATGATTATATATGGATACATTTACAAAAATAAAAAGCGGGAATTTCCCT					
	930	940	950	960	970	980
	1030					
ss.P_AAZ11186	TCGCTTGAATATT					
	*****					
ss.DNA23330	TCGCTTGAATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGA					
	990	1000	1010	1020	1030	1040
ss.DNA23330	GTAATAAATATACTTGCTTTAATTCTTAAGCATAAGTAAACATGATATAAAAATATATGC					
	1050	1060	1070	1080	1090	1100



ss.DNA23330 TGAATTACTTGTGAAGAATGCATTTAAAGCTATTTTAAATGTGTTTTATTGTAAGACA  
1110 1120 1130 1140 1150 1160

ss.DNA23330 TTACTTATTAAGAAATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCT  
1170 1180 1190 1200 1210 1220

ss.DNA23330 TAAGAATTTGCAGGTACTACAGATTTTCAAACCTGAATGAGAGAAAATTGTATAACCATC  
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<first sequence: ss.P\_AAX30168 (length = 1404)  
<second sequence: ss.DNA23330 (length = 1333)

<1321 matches in an overlap of 1333: 99.10 percent similarity  
<gaps in first sequence: 0, gaps in second sequence: 0  
<score: 3963 (match = 3, mismatch = 0, gap penalty = 8 + 1 per base)  
<endgaps not penalized

P\_AAX30168 Human secreted protein gene 24. 404 bp, DNA, PAT 18-JUN-1999  
ACCESSION P\_AAX30168  
KEYWORDS Human; secreted protein; cancer; tumour; developmental abnormality;  
foetal deficiency; blood disorder; immune system disorder;  
inflammation; autoimmune disease; allergy; Alzheimer's disease;  
cognitive disorder; schizophrenia; arthritis; asthma; psoriasis;  
sepsis; skin disorder; atherosclerosis; diabetes; cardiovascular  
disorder; kidney disorder; digestive disorder; endocrine disorder;  
infection; AIDS; patent; GENESEQ patentdb.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens.  
REFERENCE 1 (bases 1 to 1404)  
AUTHORS Fan,P., Kyaw,H., Rosen,C.A., Ruben,S.M., Wei,Y.F.  
TITLE New isolated human genes and the secreted polypeptides they encode -  
useful for diagnosis and treatment of e.g. cancers, neurological  
disorders, immune diseases, inflammation or blood disorders  
JOURNAL Patent: WO9910363-A1; Filing Date: 27-AUG-1998; 98WO-US17709;  
Publication Date: 04-MAR-1999; Priority: 29-AUG-1997;  
97US-0056271. 29-AUG-1997; 97US-0056073. 29-AUG-1997;  
97US-0056247. 29-AUG-1997; 97US-0056270; Assignee: (HUMA-) HUMAN  
GENOME SCI INC; Cross Reference: WPI; 1999-190585/16. P-PSDB;  
AAY04316; Patent Format: Claim 1; Page 145; 170pp; English.  
COMMENT AAX30145 to AAX30173 represent 29 isolated human secreted protein  
genes. AAY04293 to AAY04321 represent the secreted proteins encoded  
by the 29 human genes. The genes and their corresponding secreted  
polypeptides are useful for preventing, treating or ameliorating  
medical conditions, e.g. by protein or gene therapy. Also  
pathological conditions can be diagnosed by determining the amount  
of the new polypeptides in a sample or by determining the presence  
of mutations in the new genes. Specific uses are described for each  
of the 29 genes, based on which tissues they are most highly  
expressed in, and include developing products for the diagnosis or  
treatment of cancer, tumours, developmental abnormalities and foetal  
deficiencies, blood disorders, diseases of the immune system,  
autoimmune diseases, inflammation, allergies, Alzheimer's and  
cognitive disorders, schizophrenia, arthritis, asthma, psoriasis,  
sepsis, skin disorders, atherosclerosis, diabetes, cardiovascular  
disorders, kidney disorders, digestive/endocrine disorders,  
infections and AIDS. The polypeptides are also useful for  
identifying their binding partners. The sequences given in AAX30174  
to AAX30182 and AAY04322 to AAY04334 are used in the exemplification  
of the present invention.  
FEATURES Location/Qualifiers  
BASE COUNT 418 a 263 c 260 g 462 t 1 others  
ORIGIN  
10 20 30 40 50 60  
ss.P\_AAX30168 GTGGATCCCCGGGCTGCAGGAATTCGGCAACGGCGXCCGCTCCCCGCTCCTCCTCCCCAG  
\*\*\*  
ss.DNA23330 GCCCAGCGCTC

10

	70	80	90	100	110	120
ss.P_AAX30168	CCATGGCGTTCACGTTTCGCGGCCCTTCTGCTACATGCTGGCGCTGCTGCTCACTGCCGCGC					
ss.DNA23330	CGATGGCGTTCACGTTTCGCGGCCCTTCTGCTACATGCTGGCGCTGCTGCTCACTGCCGCGC					
	20	30	40	50	60	70
	130	140	150	160	170	180
ss.P_AAX30168	TCATCTTCTTCGCCATTTCGGCACATTATAGCATTTGATGAGCTGAAGACTGATTACAAGA					
ss.DNA23330	TCATCTTCTTCGCCATTTCGGCACATTATAGCATTTGATGAGCTGAAGACTGATTACAAGA					
	80	90	100	110	120	130
	190	200	210	220	230	240
ss.P_AAX30168	ATCCTATAGACCAGTGTAAATACCCTGAATCCCCTTGTACTCCCAGAGTACCTCATCCACG					
ss.DNA23330	ATCCTATAGACCAGTGTAAATACCCTGAATCCCCTTGTACTCCCAGAGTACCTCATCCACG					
	140	150	160	170	180	190
	250	260	270	280	290	300
ss.P_AAX30168	CTTTCTTCTGTGTCATGTTTCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATATGC					
ss.DNA23330	CTTTCTTCTGTGTCATGTTTCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATATGC					
	200	210	220	230	240	250
	310	320	330	340	350	360
ss.P_AAX30168	CCCTCTTGGCATATCATATTTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCCAGGAC					
ss.DNA23330	CCCTCTTGGCATATCATATTTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCCAGGAC					
	260	270	280	290	300	310
	370	380	390	400	410	420
ss.P_AAX30168	TCTATGACCTACAACCATCATGAATGCAGATATTCTAGCATATTGTGAGAAGGAAGGAT					
ss.DNA23330	TCTATGACCTACAACCATCATGAATGCAGATATTCTAGCATATTGTGAGAAGGAAGGAT					
	320	330	340	350	360	370
	430	440	450	460	470	480
ss.P_AAX30168	GGTGCAAATTAGCTTTTTATCTTCTAGCATTTTTTTACTACCTATATGGCATGATCTATG					
ss.DNA23330	GGTGCAAATTAGCTTTTTATCTTCTAGCATTTTTTTACTACCTATATGGCATGATCTATG					
	380	390	400	410	420	430
	490	500	510	520	530	540
ss.P_AAX30168	TTTTGGTGAGCTCTTAGAACAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAA					
ss.DNA23330	TTTTGGTGAGCTCTTAGAACAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAA					
	440	450	460	470	480	490
	550	560	570	580	590	600
ss.P_AAX30168	GCCACCAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCT					
ss.DNA23330	GCCACCAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCT					
	500	510	520	530	540	550
	610	620	630	640	650	660
ss.P_AAX30168	GATCAGTTACTTTAAAAATGACTCCTTATTTTTTAAATGTTTCCACATTTTTGCTTGTG					

```

*****
ss.DNA23330 GATCAGTTACTTTAAAAATGACTCCTTATTTTAAATGTTTCCACATTTTGTGTTGTG
              560      570      580      590      600      610

              670      680      690      700      710      720
ss.P_AAX30168 GAAAGACTGTTTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAAT
*****
ss.DNA23330 GAAAGACTGTTTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAAT
              620      630      640      650      660      670

              730      740      750      760      770      780
ss.P_AAX30168 TAATATAAAATGATTACCTCTGGTGTGACAGGTTTGAACCTGCACCTTCTTAAGGAACAG
*****
ss.DNA23330 TAATATAAAATGATTACCTCTGGTGTGACAGGTTTGAACCTGCACCTTCTTAAGGAACAG
              680      690      700      710      720      730

              790      800      810      820      830      840
ss.P_AAX30168 CCATAATCCTCTGAATGATGCATTAATTACTGACTGTCCTAGTACATTGGAAGCTTTTGT
*****
ss.DNA23330 CCATAATCCTCTGAATGATGCATTAATTACTGACTGTCCTAGTACATTGGAAGCTTTTGT
              740      750      760      770      780      790

              850      860      870      880      890      900
ss.P_AAX30168 TTATAGGAACCTTGTAGGGCTCATTTTGGTTTCATTGAAACAGTATCTAATTATAAATTAG
*****
ss.DNA23330 TTATAGGAACCTTGTAGGGCTCATTTTGGTTTCATTGAAACAGTATCTAATTATAAATTAG
              800      810      820      830      840      850

              910      920      930      940      950      960
ss.P_AAX30168 CTGTAGATATCAGGTGCTTCTGATGAAGTGAAAATGTATATCTGACTAGTGGGAACTTC
*****
ss.DNA23330 CTGTAGATATCAGGTGCTTCTGATGAAGTGAAAATGTATATCTGACTAGTGGGAACTTC
              860      870      880      890      900      910

              970      980      990      1000      1010      1020
ss.P_AAX30168 ATGGGTTTCCTCATCTGTCATGTCGATGATTATATATGGATACATTTACAAAAATAAAAA
*****
ss.DNA23330 ATGGGTTTCCTCATCTGTCATGTCGATGATTATATATGGATACATTTACAAAAATAAAAA
              920      930      940      950      960      970

              1030      1040      1050      1060      1070      1080
ss.P_AAX30168 GCGGGAATTTTCCCTTCGCTTGAATATTATCCCTGTATATTGCATGAATGAGAGATTTCC
*****
ss.DNA23330 GCGGGAATTTTCCCTTCGCTTGAATATTATCCCTGTATATTGCATGAATGAGAGATTTCC
              980      990      1000      1010      1020      1030

              1090      1100      1110      1120      1130      1140
ss.P_AAX30168 CATATTTCCATCAGAGTAATAAATATACTTGCTTTAATTCTTAAGCATAAGTAAACATGA
*****
ss.DNA23330 CATATTTCCATCAGAGTAATAAATATACTTGCTTTAATTCTTAAGCATAAGTAAACATGA
              1040      1050      1060      1070      1080      1090

              1150      1160      1170      1180      1190      1200
ss.P_AAX30168 TATAAAATATATGCTGAATTACTTGTGAAGAATGCATTTAAAGCTATTTTAAATGTGTT
*****
ss.DNA23330 TATAAAATATATGCTGAATTACTTGTGAAGAATGCATTTAAAGCTATTTTAAATGTGTT
              1100      1110      1120      1130      1140      1150

```

	1210	1220	1230	1240	1250	1260
ss.P_AAX30168	TTTATTTGTAAGACATTACTTATTAAGAAATTGGTTATTATGCTTACTGTTCTAATCTGG					
	*****					
ss.DNA23330	TTTATTTGTAAGACATTACTTATTAAGAAATTGGTTATTATGCTTACTGTTCTAATCTGG					
	1160	1170	1180	1190	1200	1210
	1270	1280	1290	1300	1310	1320
ss.P_AAX30168	TGGTAAAGGTATTCTTAAGAATTTGCAGGTACTACAGATTTTCAAACCTGAATGAGAGAA					
	*****					
ss.DNA23330	TGGTAAAGGTATTCTTAAGAATTTGCAGGTACTACAGATTTTCAAACCTGAATGAGAGAA					
	1220	1230	1240	1250	1260	1270
	1330	1340	1350	1360	1370	1380
ss.P_AAX30168	AATTGTATAACCATCCTGCTGTTCCCTTTAGTGCAATACAATAAACTCTGAAATTAAC					
	*****					
ss.DNA23330	AATTGTATAACCATCCTGCTGTTCCCTTTAGTGCAATACAATAAACTCTGAAATTAAGAC					
	1280	1290	1300	1310	1320	1330
	1390	1400				
ss.P_AAX30168	AAAAAAAAAAAAAAAAAACTCGTA					
ss.DNA23330	TC					

<first sequence: ss.AA902726 (length = 500)  
 <second sequence: ss.DNA23330 (length = 1333)  
 <240 matches in an overlap of 500: 48.00 percent similarity  
 <gaps in first sequence: 6 (151 bases), gaps in second sequence: 1 (7 bases)  
 <score: 606 (match = 3, mismatch = 0, gap penalty = 8 + 1 per base)  
 <endgaps not penalized

GenBank (Release 135, apr 2003) [May 6 09:17:26 2003]:

AA902726 ok71h07.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA clone IMAGE:1519453 3',  
 mRNA sequence. 500 bp, mRNA, linear, EST 09-JUN-1998  
 ACCESSION AA902726  
 VERSION AA902726.1 GI:3037849  
 KEYWORDS EST; NCI\_est; 3\_prime.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 REFERENCE 1 (bases 1 to 500)  
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT High quality stops: 375; insert: 1413.  
 FEATURES  
 source Location/Qualifiers

1..500  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1519453"  
 /clone\_lib="NCI\_CGAP\_GC4"  
 /tissue\_type="pooled germ cell tumors"  
 /lab\_host="DH10B"  
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
 polylinker; 1st strand cDNA was prepared from 3 pooled  
 germ cell tumors, and was then primed with a Not I -  
 oligo(dT) primer. Double-stranded cDNA was ligated to Eco  
 RI adaptors (Pharmacia), digested with Not I and cloned  
 into the Not I and Eco RI sites of the modified pT7T3  
 vector. Library is normalized. Library was constructed by  
 Bento Soares and M. Fatima Bonaldo."

BASE COUNT  
 ORIGIN

180 a 81 c 66 g 173 t

ss.DNA23330 GCCCACGCGTCCGATGGCGTTCACGTTTCGCGGCCTTCTGCTACATGCTGGCGCTGCTGCT  
 10 20 30 40 50 60  
 ss.DNA23330 CACTGCCGCGCTCATCTTCTTCGCCATTTGGCACATTATAGCATTTGATGAGCTGAAGAC  
 70 80 90 100 110 120  
 ss.DNA23330 TGATTACAAGAATCCTATAGACCAGTGTAAATACCCTGAATCCCCTTGTA TCTCCAGAGTA  
 130 140 150 160 170 180  
 ss.DNA23330 CCTCATCCACGCTTTCTTCTGTGTCATGTTTCTTGTGTCAGCAGAGTGGCTTACACTGGG  
 190 200 210 220 230 240  
 ss.DNA23330 TCTCAATATGCCCCCTCTTGGCATATCATATTTGGAGGTATATGAGTAGACCAGTGATGAG  
 250 260 270 280 290 300  
 ss.DNA23330 TGGCCCAGGACTCTATGACCCTACAACCATCATGAATGCAGATATTCTAGCATATTGTCA

	310	320	330	340	350	360
ss.DNA23330	GAAGGAAGGATGGTGCAAATTAGCTTTTTATCTTCTAGCATTTTTTTACTACCTATATGG					
	370	380	390	400	410	420
ss.AA902726	10	20	30	40	50	
	TAATTTTCAGAGTTTATTGTATTGCACTAAAGGAACAGCAGGA-TGGTTATACAATTT					
	* * * * *					
ss.DNA23330	CATGATCTATGTTTTGGTGAGCTCTTAGAACAACACAGAGAAGAAATTGGTCCAGTTAAGT					
	430	440	450	460	470	480
ss.AA902726	60	70	80	90	100	110
	TCTCTCATTTCAGTTTTGAAAATCTG----TAGTACCTGCAAATTCTTAAGAATACCTTTA					
	* * * * *					
ss.DNA23330	GCATGCAAAAAGCCACCAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGC					
	490	500	510	520	530	540
ss.AA902726	120	130	140	150	160	170
	CCACCAGATTAGAACAGTAAGCATAATAACCAATTTCTTAATAAGTAATGTCTTACAAAT					
	* * * * *					
ss.DNA23330	CTGTGGAATCTGATCAGTTACTTTAAAAAATGACTCCTTATTTTTTAAATGTTTCCACAT					
	550	560	570	580	590	600
ss.AA902726	180	190	200	210		
	-----AAAAACACATTTAAAA---TAGCTTTAAATGCATTCTTCACAAGTAAT					
	* * * * *					
ss.DNA23330	TTTTGCTTGTGGAAAGACTGTTTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTAT					
	610	620	630	640	650	660
ss.AA902726	220	230	240	250		
	TCAGCATATATTTTATATCATGTTTACTTATGCT-----					
	* * * * *					
ss.DNA23330	TACGTATAAATTAATATAAAATGATTACCTCTGGTGTGACAGGTTTGAACCTTGCACTTC					
	670	680	690	700	710	720
ss.AA902726	-----					
ss.DNA23330	TTAAGGAACAGCCATAATCCTCTGAATGATGCATTAATTACTGACTGTCCTAGTACATTG					
	730	740	750	760	770	780
ss.AA902726				260	270	
	-----TAAGAATTAAAGCAAGTATAT					
	* * * * *					
ss.DNA23330	GAAGCTTTTGTATTATAGGAACCTTGTAGGGCTCATTTTGGTTTCATTGAAACAGTATCTAA					
	790	800	810	820	830	840
ss.AA902726	280	290	300	310	320	330
	TTATTACTCTGATGGAAATATGGGAAATCTCTCATTCATGCAATATACAGGGATAATATT					
	* * * * *					
ss.DNA23330	TTATAAATTAGCTGTAGATATCAGGTGCTTCTGATGAAGTGAAAT-----GTATATC					
	850	860	870	880	890	
ss.AA902726	340	350	360	370	380	390
	CAAGCGAAGGGAAAATTCCTGCTTTTTATTTTTGTAAATGTATCCATATATAATCATCGA					
	* * * * *					
ss.DNA23330	TGACTAGTGGGAAACTTCATGGGTTTCCTCATCTGTCATGTCGATGATTATATATGGATA					
	900	910	920	930	940	950

	400	410	420	430	440
ss.AA902726	CATGACAGATGAGGAAACCCATGAAGTTTCCCACTAGTCAGATA-----TACATTTTC				
	*** *				
ss.DNA23330	CATTTACAAAAATAAAAAGCGGGAATTTTCCCTTCGCTTGAATATTATCCCTGTATATTG				
	960	970	980	990	1000 1010
	450	460	470	480	490 500
ss.AA902726	ACTTCATCAGAAGCACCTGATATCTACAGCTAATTTATAATTAGATACTGTTT				
	* *				
ss.DNA23330	CATGAATGAGAGATTTCCCATATTTCCATCAGAGTAATAAATATACTTGCTTTAATTCTT				
	1020	1030	1040	1050	1060 1070
ss.DNA23330	AAGCATAAGTAAACATGATATAAAAATATATGCTGAATTACTTGTGAAGAATGCATTTAA				
	1080	1090	1100	1110	1120 1130
ss.DNA23330	AGCTATTTTAAATGTGTTTTTATTTGTAAGACATTACTTATTAAGAAATTGGTTATTATG				
	1140	1150	1160	1170	1180 1190
ss.DNA23330	CTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAGAATTTGCAGGTACTACAGATTTT				
	1200	1210	1220	1230	1240 1250
ss.DNA23330	CAAAACTGAATGAGAGAAAATTGTATAACCATCCTGCTGTTCCCTTTAGTGCAATACAATA				
	1260	1270	1280	1290	1300 1310
ss.DNA23330	AAACTCTGAAATTAAGACTC				
	1320	1330			



<first sequence: ss.AA689524 (length = 544)  
<second sequence: ss.DNA23330 (length = 1333)

<544 matches in an overlap of 544: 100.00 percent similarity  
<gaps in first sequence: 1 (1 base), gaps in second sequence: 0  
<score: 1623 (match = 3, mismatch = 0, gap penalty = 8 + 1 per base)  
<endgaps not penalized

GenBank (Release 135, apr 2003)[May 6 08:58:44 2003]:

AA689524 ns66e01.r1 NCI\_CGAP\_Pr22 Homo sapiens cDNA clone IMAGE:1188600 5'  
similar to SW:CNI\_DROME P49858 CORNICHON PROTEIN. ; , mRNA sequence.  
544 bp, mRNA, linear, EST 24-DEC-1997

ACCESSION AA689524  
VERSION AA689524.1 GI:2689871  
KEYWORDS EST; NCI\_est; 5\_prime.  
SOURCE Homo sapiens (human).  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 544)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT High quality stops: 499; insert: 484.  
FEATURES Location/Qualifiers  
source 1..544  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1188600"  
/clone\_lib="NCI\_CGAP\_Pr22"  
/sex="male"  
/tissue\_type="normal prostate"  
/lab\_host="DH10B"  
/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)  
with a modified polylinker; 1st strand cDNA was prepared  
from normal prostate bulk tissue, and was then primed with  
a Not I - oligo(dT) primer. Double-stranded cDNA was  
ligated to Eco RI adaptors (Pharmacia), digested with Not  
I and cloned into the Not I and Eco RI sites of the  
modified pT7T3 vector. Library is normalized, and was  
constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 165 a 91 c 103 g 185 t  
ORIGIN

ss.DNA23330 GCCCACGCGTCCGATGGCGTTCACGTTTCGCGGCCTTCTGCTACATGCTGGCGCTGCTGCT  
10 20 30 40 50 60

ss.DNA23330 CACTGCCGCGCTCATCTTCTTCGCCATTTGGCACATTATAGCATTGTGATGAGCTGAAGAC  
70 80 90 100 110 120

ss.DNA23330 TGATTACAAGAATCCTATAGACCAGTGTAAATACCCTGAATCCCCCTGTACTCCAGAGTA  
130 140 150 160 170 180

ss.DNA23330 CCTCATCCACGCTTTCTTCTGTGTCATGTTTCTTTGTGCAGCAGAGTGGCTTACACTGGG  
190 200 210 220 230 240

ss.AA689524 GTGATGAG

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ss.DNA23330 TCTCAATATGCCCCCTCTTGGCATATCATATTTGGAGGTATATGAGTAGACCAGTGATGAG
                250      260      270      280      290      300

ss.AA689524 10      20      30      40      50      60
TGG-CCAGGACTCTATGACCCTACAACCATCATGAATGCAGATATTCTAGCATATTGTCA
*** *****

ss.DNA23330 TGGCCCAGGACTCTATGACCCTACAACCATCATGAATGCAGATATTCTAGCATATTGTCA
                310      320      330      340      350      360

ss.AA689524 70      80      90      100     110     120
GAAGGAAGGATGGTGCAAATTAGCTTTTTATCTTCTAGCATTTTTTTTACTACCTATATGG
*****

ss.DNA23330 GAAGGAAGGATGGTGCAAATTAGCTTTTTATCTTCTAGCATTTTTTTTACTACCTATATGG
                370      380      390      400      410      420

ss.AA689524 130     140     150     160     170     180
CATGATCTATGTTTTGGTGAGCTCTTAGAACAACACACAGAAGAATTGGTCCAGTTAAGT
*****

ss.DNA23330 CATGATCTATGTTTTGGTGAGCTCTTAGAACAACACACAGAAGAATTGGTCCAGTTAAGT
                430     440     450     460     470     480

ss.AA689524 190     200     210     220     230     240
GCATGCAAAAAGCCACCAAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGC
*****

ss.DNA23330 GCATGCAAAAAGCCACCAAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGC
                490     500     510     520     530     540

ss.AA689524 250     260     270     280     290     300
CTGTGGAATCTGATCAGTTACTTTAAAAAATGACTCCTTATTTTTTAAATGTTTCCACAT
*****

ss.DNA23330 CTGTGGAATCTGATCAGTTACTTTAAAAAATGACTCCTTATTTTTTAAATGTTTCCACAT
                550     560     570     580     590     600

ss.AA689524 310     320     330     340     350     360
TTTTGCTTGTTGGAAAGACTGTTTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTAT
*****

ss.DNA23330 TTTTGCTTGTTGGAAAGACTGTTTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTAT
                610     620     630     640     650     660

ss.AA689524 370     380     390     400     410     420
TACGTATAAAATTAATATAAAATGATTACCTCTGGTGTTGACAGGTTTGAACCTGCACTTC
*****

ss.DNA23330 TACGTATAAAATTAATATAAAATGATTACCTCTGGTGTTGACAGGTTTGAACCTGCACTTC
                670     680     690     700     710     720

ss.AA689524 430     440     450     460     470     480
TTAAGGAACAGCCATAATCCTCTGAATGATGCATTAATTACTGACTGTCCTAGTACATTG
*****

ss.DNA23330 TTAAGGAACAGCCATAATCCTCTGAATGATGCATTAATTACTGACTGTCCTAGTACATTG
                730     740     750     760     770     780

ss.AA689524 490     500     510     520     530     540
GAAGCTTTTGTATTATAGGAACCTGTAGGGCTCATTTTGGTTTCATTGAAACAGTATC
*****

ss.DNA23330 GAAGCTTTTGTATTATAGGAACCTGTAGGGCTCATTTTGGTTTCATTGAAACAGTATCTAA
                790     800     810     820     830     840

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ss.DNA23330 TTATAAATTAGCTGTAGATATCAGGTGCTTCTGATGAAGTGAAAAATGTATATCTGACTAG  
                   850          860          870          880          890          900

ss.DNA23330 TGGGAAACTTCATGGGTTTCCTCATCTGTCATGTCGATGATTATATATGGATACATTTAC  
                   910          920          930          940          950          960

ss.DNA23330 AAAAATAAAAAGCGGGAATTTTCCTTCGCTTGAATATTATCCCTGTATATTGCATGAAT  
                   970          980          990          1000         1010         1020

ss.DNA23330 GAGAGATTTCCTATATTTCCATCAGAGTAATAAATATACTTGCTTTAATTCTTAAGCATA  
                   1030         1040         1050         1060         1070         1080

ss.DNA23330 AGTAAACATGATATAAAAAATATATGCTGAATTACTTGTGAAGAATGCATTTAAAGCTATT  
                   1090         1100         1110         1120         1130         1140

ss.DNA23330 TTAAATGTGTTTTTATTTGTAAGACATTACTTATTAAGAAATTGGTTATTATGCTTACTG  
                   1150         1160         1170         1180         1190         1200

ss.DNA23330 TTCTAATCTGGTGGTAAAGGTATTCTTAAGAATTTGCAGGTACTACAGATTTTCAAACCT  
                   1210         1220         1230         1240         1250         1260

ss.DNA23330 GAATGAGAGAAAAATTGTATAACCATCCTGCTGTTTCCTTTAGTGCAATACAATAAAACTCT  
                   1270         1280         1290         1300         1310         1320

ss.DNA23330 GAAATTAAGACTC  
                   1330

<first sequence: ss.P\_AAX90853 (length = 1378)

<second sequence: ss.DNA23330 (length = 1333)

<1325 matches in an overlap of 1333: 99.40 percent similarity

<gaps in first sequence: 0, gaps in second sequence: 0

<score: 3975 (match = 3, mismatch = 0, gap penalty = 8 + 1 per base)

<endgaps not penalized

GenBank (Release 135, apr 2003)[May 6 11:26:58 2003]:

P\_AAX90853 cDNA clone pk65\_4. 378 bp, DNA, PAT 17-JAN-2000  
ACCESSION P\_AAX90853  
KEYWORDS clone pk65\_4; pk65\_4 protein; human foetal kidney cDNA library;  
secreted protein; gene therapy; cytokine; nutritional activity;  
tissue growth; cell proliferation; immune stimulation; immune  
suppression; hematopoiesis regulation; tumour inhibition; patent;  
GENESEQ patentdb.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens.  
REFERENCE 1 (bases 1 to 1378)  
AUTHORS Jacobs,K., Mccoy,J.M., LaVallie,E.R., Collins-Racie,L.A.,  
Evans,C. Merberg,D., Treacy,M., Agostino,M.J., Steininger,R.J.  
TITLE Polynucleotides encoding secreted human proteins, derived from human  
adult brain, human fetal brain, human fetal kidney, and human adult  
blood cDNA libraries -  
JOURNAL Patent: WO9950405-A1; Filing Date: 30-MAR-1999; 99WO-US06946;  
Publication Date: 07-OCT-1999; Priority: 31-MAR-1998;  
98US-0080110. 29-MAR-1999; 99US-0280591; Assignee: (GEMY )  
GENETICS INST INC; Cross Reference: WPI; 1999-610849/52. P-PSDB;  
AAY28813; Patent Format: Claim 20; Page 104-105; 122pp; English.  
COMMENT The present nucleotide sequence comprises the full-length  
protein-coding sequence of clone pk65\_4. pk65\_4 was isolated from a  
human foetal kidney cDNA library using methods specific for secreted  
protein cDNAs. This can be used in gene therapy. The polynucleotide  
and protein may effect nutritional activity, cytokine and cell  
proliferation, immune stimulation or suppression, hematopoiesis  
regulation, tissue growth, tumour inhibition etc.  
FEATURES Location/Qualifiers  
CDS 44..478  
/\*tag= a  
/product= "pk65\_4 protein"  
BASE COUNT 411 a 258 c 252 g 457 t  
ORIGIN  
10 20 30 40 50 60  
ss.P\_AAX90853 CTCCGCTGGCAACGGCGCCGCTCCCCGCTCCTCCTCCCCAGCCATGGCGTTCACGTTTCGC  
\* \* \* \* \*  
ss.DNA23330 GCCCACGCGTCCGATGGCGTTCACGTTTCGC  
10 20 30  
70 80 90 100 110 120  
ss.P\_AAX90853 GGCCTTCTGCTACATGCTGGCGCTGCTGCTCACTGCCGCGCTCATCTTCTTCGCCATTTG  
\*\*\*\*\*  
ss.DNA23330 GGCCTTCTGCTACATGCTGGCGCTGCTGCTCACTGCCGCGCTCATCTTCTTCGCCATTTG  
40 50 60 70 80 90  
130 140 150 160 170 180  
ss.P\_AAX90853 GCACATTATAGCATTTGATGAGCTGAAGACTGATTACAAGAATCCTATAGACCAGTGTA

```

*****
ss.DNA23330 GCACATTATAGCATTTGATGAGCTGAAGACTGATTACAAGAATCCTATAGACCAGTGTA
              100      110      120      130      140      150

              190      200      210      220      230      240
ss.P_AAX90853 TACCCTGAATCCCCTTGTACTCCCAGAGTACCTCATCCACGCTTTCTTCTGTGTCATGTT
*****
ss.DNA23330 TACCCTGAATCCCCTTGTACTCCCAGAGTACCTCATCCACGCTTTCTTCTGTGTCATGTT
              160      170      180      190      200      210

              250      260      270      280      290      300
ss.P_AAX90853 TCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATATGCCCCCTCTTGGCATATCATAT
*****
ss.DNA23330 TCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATATGCCCCCTCTTGGCATATCATAT
              220      230      240      250      260      270

              310      320      330      340      350      360
ss.P_AAX90853 TTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCCAGGACTCTATGACCCTACAACCAT
*****
ss.DNA23330 TTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCCAGGACTCTATGACCCTACAACCAT
              280      290      300      310      320      330

              370      380      390      400      410      420
ss.P_AAX90853 CATGAATGCAGATATTCTAGCATATTGTGAGAAGGAAGGATGGTGCAAATTAGCTTTTTA
*****
ss.DNA23330 CATGAATGCAGATATTCTAGCATATTGTGAGAAGGAAGGATGGTGCAAATTAGCTTTTTA
              340      350      360      370      380      390

              430      440      450      460      470      480
ss.P_AAX90853 TCTTCTAGCATTTTTTTTACTACCTATATGGCATGATCTATGTTTTGGTGAGCTCTTAGAA
*****
ss.DNA23330 TCTTCTAGCATTTTTTTTACTACCTATATGGCATGATCTATGTTTTGGTGAGCTCTTAGAA
              400      410      420      430      440      450

              490      500      510      520      530      540
ss.P_AAX90853 CAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAAGCCACCAAATGAAGGGATT
*****
ss.DNA23330 CAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAAGCCACCAAATGAAGGGATT
              460      470      480      490      500      510

              550      560      570      580      590      600
ss.P_AAX90853 CTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGTTACTTTAAAAAA
*****
ss.DNA23330 CTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGTTACTTTAAAAAA
              520      530      540      550      560      570

              610      620      630      640      650      660
ss.P_AAX90853 TGACTCCTTATTTTTTAAATGTTTCCACATTTTGCTTGTGGAAAGACTGTTTTCATATG
*****
ss.DNA23330 TGACTCCTTATTTTTTAAATGTTTCCACATTTTGCTTGTGGAAAGACTGTTTTCATATG
              580      590      600      610      620      630

              670      680      690      700      710      720
ss.P_AAX90853 TTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAATTAATATAAAATGATTACCT
*****
ss.DNA23330 TTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAATTAATATAAAATGATTACCT
              640      650      660      670      680      690

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	730	740	750	760	770	780
ss.P_AAX90853	CTGGTGTGACAGGTTTGAACCTTGCACTTCTTAAGGAACAGCCATAATCCTCTGAATGAT					
	*****					
ss.DNA23330	CTGGTGTGACAGGTTTGAACCTTGCACTTCTTAAGGAACAGCCATAATCCTCTGAATGAT					
	700	710	720	730	740	750
	790	800	810	820	830	840
ss.P_AAX90853	GCATTAATTACTGACTGTCCTAGTACATTGGAAGCTTTTGTGTTATAGGAACCTGTAGGGC					
	*****					
ss.DNA23330	GCATTAATTACTGACTGTCCTAGTACATTGGAAGCTTTTGTGTTATAGGAACCTGTAGGGC					
	760	770	780	790	800	810
	850	860	870	880	890	900
ss.P_AAX90853	TCATTTTGGTTTCATTGAAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGTGCTT					
	*****					
ss.DNA23330	TCATTTTGGTTTCATTGAAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGTGCTT					
	820	830	840	850	860	870
	910	920	930	940	950	960
ss.P_AAX90853	CTGATGAAGTGAAAATGTATATCTGACTAGTGGGAAAC TTCATGGGTTTCCTCATCTGTC					
	*****					
ss.DNA23330	CTGATGAAGTGAAAATGTATATCTGACTAGTGGGAAAC TTCATGGGTTTCCTCATCTGTC					
	880	890	900	910	920	930
	970	980	990	1000	1010	1020
ss.P_AAX90853	ATGTCGATGATTATATATGGATACATTTACAAAAATAAAAAGCGGGAATTTTCCCTTCGC					
	*****					
ss.DNA23330	ATGTCGATGATTATATATGGATACATTTACAAAAATAAAAAGCGGGAATTTTCCCTTCGC					
	940	950	960	970	980	990
	1030	1040	1050	1060	1070	1080
ss.P_AAX90853	TTGAATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGAGTAA					
	*****					
ss.DNA23330	TTGAATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGAGTAA					
	1000	1010	1020	1030	1040	1050
	1090	1100	1110	1120	1130	1140
ss.P_AAX90853	TAAATATACTTGCTTTAATTCTTAAGCATAAGTAAACATGATATAAAAAATATATGCTGAA					
	*****					
ss.DNA23330	TAAATATACTTGCTTTAATTCTTAAGCATAAGTAAACATGATATAAAAAATATATGCTGAA					
	1060	1070	1080	1090	1100	1110
	1150	1160	1170	1180	1190	1200
ss.P_AAX90853	TTACTTGTGAAGAAATGCATTTAAAGCTATTTTAAATGTGTTTTTATTTGTAAGACATTAC					
	*****					
ss.DNA23330	TTACTTGTGAAGAAATGCATTTAAAGCTATTTTAAATGTGTTTTTATTTGTAAGACATTAC					
	1120	1130	1140	1150	1160	1170
	1210	1220	1230	1240	1250	1260
ss.P_AAX90853	TTATTAAGAAATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAG					
	*****					
ss.DNA23330	TTATTAAGAAATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAG					
	1180	1190	1200	1210	1220	1230
	1270	1280	1290	1300	1310	1320
ss.P_AAX90853	AATTTGCAGGTACTACAGATTTTCAAACTGAATGAGAGAAAATTGTATAACCATCCTGC					
	*****					
ss.DNA23330	AATTTGCAGGTACTACAGATTTTCAAACTGAATGAGAGAAAATTGTATAACCATCCTGC					

	1240	1250	1260	1270	1280	1290
	1330	1340	1350	1360	1370	
ss.P_AAX90853	TG TTC CTT TAG TGC AAT ACA ATA AACT CTG AAATTA AGACT CAAAAAAAAAAAAAAAAA					
	*****					
ss.DNA23330	TG TTC CTT TAG TGC AAT ACA ATA AACT CTG AAATTA AGACT C					
	1300	1310	1320	1330		

L2 ANSWER 1 OF 1 MEDLINE on STN  
 AN 1999227056 MEDLINE  
 DN 99227056 PubMed ID: 10209299  
 TI The **human homolog** of **Drosophila**  
**cornichon** protein is differentially expressed in alloactivated  
 T-cells.  
 AU Utku N; Bulwin G C; Beinke S; Heinemann T; Beato F; Randall J; Schnieders  
 B; Sandhoff K; Volk H D; Milford E; Gullans S R  
 CS Institut fur Medizinische Immunologie, Campus Mitte, Charite, Humboldt  
 Universitat, Schumannstrasse 20/21, 10098, Berlin, Germany..  
 nalan.utku@charite.de  
 NC DK36031 (NIDDK)  
 SO BIOCHIMICA ET BIOPHYSICA ACTA, (1999 Apr 1) 1449 (3) 203-10.  
 Journal code: 0217513. ISSN: 0006-3002.  
 CY Netherlands  
 DT Journal; Article; (JOURNAL ARTICLE)  
 LA English  
 FS Priority Journals  
 OS GENBANK-AF022811; GENBANK-AF031379  
 EM 199905  
 ED Entered STN: 19990607  
 Last Updated on STN: 19990607  
 Entered Medline: 19990525  
 AB To identify novel genes induced in the early stage of T-cell activation,  
 mRNA expression in alloactivated human lymphocytes was examined.  
 Differential display-reverse transcription PCR analysis revealed a 207-bp  
 cDNA fragment which was upregulated 24 h after allostimulation of a human  
 T-cell line. The corresponding complete 1396 bp cDNA, named TGAM77,  
 encodes a predicted 134 amino acid protein which shares 63% homology with  
 the cornichon (cni) protein of *Drosophila melanogaster*. Upregulation of  
 TGAM77 mRNA in the early phase of T-cell activation was confirmed by  
 Northern blot and RT-PCR analysis of activated human lymphocytes. TGAM77  
 mRNA is expressed in a variety of human tissues with various expression  
 levels. In analogy to cni which is involved in an epidermal growth  
 factor-like signaling pathway inducing cellular asymmetry in *Drosophila*  
 oogenesis, TGAM77 might function in similar signaling establishing  
 vectorial re-localization and concentration of signaling events in T-cell  
 activation.



L1 ANSWER 1 OF 1 MEDLINE on STN  
 AN 2001401135 MEDLINE  
 DN 21347415 PubMed ID: 11455434  
 TI **Isolation of genes involved in**  
**ascidian metamorphosis:** epidermal growth factor  
 signaling and metamorphic competence.  
 AU Davidson B; Swalla B J  
 CS Zoology Department and Center for Developmental Biology, University of  
 Washington, Box 351800, Seattle, WA 98195-1800, USA.  
 SO DEVELOPMENT GENES AND EVOLUTION, (2001 Apr) 211 (4) 190-4.  
 Journal code: 9613264. ISSN: 0949-944X.  
 CY Germany: Germany, Federal Republic of  
 DT Journal; Article; (JOURNAL ARTICLE)  
 LA English  
 FS Priority Journals  
 EM 200110  
 ED Entered STN: 20011029  
 Last Updated on STN: 20011029  
 Entered Medline: 20011025  
 AB Although embryonic development in ascidians has been studied for over a  
 century, the signals involved in coordinating post-larval development and  
 metamorphosis are just beginning to be investigated. In this paper, we  
 demonstrate that transcription is necessary for both the acquisition of  
 metamorphic competence and the completion of the initial events of  
 metamorphosis in *Boltenia villosa*. Transcripts expressed during  
 metamorphic competence were isolated by a suppressive PCR subtraction of  
*Boltenia villosa* larval cDNAs. One of these transcripts is homologous to  
 cornichon. Cornichon has a crucial but undefined role in epidermal growth  
 factor (EGF) signaling during *Drosophila* embryogenesis. In situ  
 hybridization demonstrates that *Boltenia* cornichon (Cnib) is expressed in  
 the anterior papillary region of larvae as they gain competence. Our  
 hypothesis is that Cnib acts to potentiate EGF signaling, thereby allowing  
*Boltenia* larvae to respond to cues for metamorphosis. Further research  
 into the role of Cnib in urochordate metamorphosis may provide insight  
 into the function of cornichon in other organisms. A better molecular  
 understanding of urochordate metamorphosis will also provide a foundation  
 for exploring the role of metamorphosis in chordate evolution.